AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows.

Please replace paragraph [0052] on page 13 with the following amended paragraph:

[0052] The term "variant" refers to polynucleotides or polypeptides of the invention modified at one or more base pairs, codons, introns, exons, or amino acid residues (respectively) yet still retain the biological activity of an amidase of the invention. Variants can be produced by any number of means included methods such as, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturated Mutagenesis™ ~~gene site saturated mutagenesis~~ (GSSM™) and any combination thereof.

Please replace paragraph [0101] on page 29 with the following amended paragraph:

[0101] As representative examples of expression vectors which may be used, there may be mentioned viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (*e.g.*, vaccinia, adenovirus, foul pox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as *Bacillus, Aspergillus* ~~bacillus, aspergillus~~ and yeast). Thus, for example, the DNA may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example; Bacterial: pQE vectors (Qiagen), ~~pBluescript~~ pBLUESCRIPT™ (Stratagene, San Diego, CA) plasmids, pNH vectors, (lambda-ZAP vectors (Stratagene); ptrc99a, pKK223-3,

pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene), pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia). However, any other plasmid or other vector may be used so long as they are replicable and viable in the host. Low copy number or high copy number vectors may be employed with the present invention.

Please replace paragraph [0116] on page 35 with the following amended paragraph:

[0116] The invention also provides for the use of proprietary codon primers (containing a degenerate N,N,N sequence) to introduce point mutations into a polynucleotide, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position (Gene Site Saturated Mutagenesis™ ~~gene site saturated mutagenesis~~ (GSSM™)). The oligos used are comprised contiguously of a first homologous sequence, a degenerate N,N,N sequence, and preferably but not necessarily a second homologous sequence. The downstream progeny translational products from the use of such oligos include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,N sequence includes codons for all 20 amino acids.

Please replace paragraph [0165] on page 51 with the following amended paragraph:

[0165] Particular bacterial vectors which may be used include the commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017), pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden), GEM1 (Promega Biotec, Madison, WI, USA) pQE70, pQE60, pQE-9 (Qiagen), pD10, psiX174, ~~pBluescript~~ pBLUESCRIPT II KS™, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene), ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), pKK232-8 and pCM7. Particular eukaryotic vectors include pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). However, any other vector may be used as long as it is replicable and viable in the host cell.

Please replace paragraph [0197] on page 61 with the following amended paragraph:

[0197] SEQ ID NO:2, and sequences substantially identical thereto or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in a variety of applications. For example, the polypeptides or fragments thereof may be used to catalyze biochemical reactions. In accordance with one aspect of the invention, there is provided a process for utilizing SEQ ID NO:2, and sequences substantially identical thereto or polynucleotides encoding such polypeptides for hydrolyzing glycosidic linkages. ~~In such procedures, a substance containing a glycosidic linkage (*e.g.*, a starch) is contacted with SEQ ID NO:2, or sequences substantially identical thereto under conditions which facilitate the hydrolysis of the glycosidic linkage.~~

Please replace paragraph [0246] on page 80 with the following amended paragraph:

[0246] The programs and databases which may be used include, but are not limited to: MACPATTERN ~~MacPattern~~ (EMBL), DISCOVERYBASE ~~DiscoveryBase~~ (Molecular Applications Group), GENEMINE ~~GeneMine~~ (Molecular Applications Group), LOOK ~~Look~~ (Molecular Applications Group), MACLOOK ~~MacLook~~ (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul et al, J. Mol. Biol. 215: 403, 1990), FASTA (Pearson and Lipman, Proc. Natl. Acad. Sci. USA, 85: 2444, 1988), FASTDB (Brutlag *et al.* Comp. App. Biosci. 6:237-245, 1990), CATALYST ~~Catalyst~~ (Molecular Simulations Inc.), CATALYST ~~Catalyst~~ /SHAPE (Molecular Simulations Inc.), CERIUS^2.DBACCESS ~~Cerius^2.DBAccess~~ (Molecular Simulations Inc.), HYPOGEN ~~HypoGen~~ (Molecular Simulations Inc.), INSIGHT ~~Insight~~ II, (Molecular Simulations Inc.), DISCOVER ~~Discover~~ (Molecular Simulations Inc.), CHARMm (Molecular Simulations Inc.), FELIX ~~Felix~~ (Molecular Simulations Inc.), DELPHI ~~DelPhi~~, (Molecular Simulations Inc.), QUANTEMM ~~QuanteMM~~, (Molecular Simulations Inc.), HOMOLOGY ~~Homology~~ (Molecular Simulations Inc.), MODELER

~~Modeler~~ (Molecular Simulations Inc.), ISIS (Molecular Simulations Inc.), QUANTA/PROTEIN DESIGN ~~Quanta/Protein Design~~ (Molecular Simulations Inc.), WEBLAB ~~WebLab~~ (Molecular Simulations Inc.), WEBLAB ~~WebLab~~ Diversity Explorer (Molecular Simulations Inc.), GENE EXPLORER ~~Gene Explorer~~ (Molecular Simulations Inc.), SEQFOLD ~~SeqFold~~ (Molecular Simulations Inc.), the MDL Available Chemicals Directory database, the MDL Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwent's World Drug Index database, the BioByteMasterFile database, the Genbank database, and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure.

Please replace paragraph [0258] on page 84 with the following amended paragraph:

[0258] Colonies containing ~~pBluescript~~ pBLUESCRIPT™ plasmids with random inserts from the organism Thermococcus GU5L5 was obtained according to the method of Hay and Short. (Hay, B. and Short, J., Strategies. 1992, 5, 16.) The resulting colonies were picked with sterile toothpicks and used to singly inoculate each of the wells of 96-well microtiter plates. The wells contained 250 µL of LB media with 100 µg/mL ampicillin, 80 µg/mL methicillin, and 10% v/v glycerol (LB Amp/Meth, glycerol). The cells were grown overnight at 37° C. without shaking. This constituted generation of the "SourceGenBank" ~~"SourceGeneBank"~~; each well of the Source GenBank ~~GeneBank~~ thus contained a stock culture of *E. coli* cells, each of which contained a pBluescript plasmid with a unique DNA insert.

Please replace paragraph [0259] on page 84 with the following amended paragraph:

[0259] The plates of the Source GenBank ~~GeneBank~~ were used to multiply inoculate a single plate (the "Condensed Plate") containing in each well 200 µL of LB Amp/Meth, glycerol. This step was performed using the High Density Replicating Tool (HDRT) of the Beckman BIOMEK™ (Beckman Coulter, Inc., Fullerton, CA) ~~Biomek~~ with a 1%

bleach, water, isopropanol, air-dry sterilization cycle in between each inoculation. Each well of the Condensed Plate thus contained 10 to 12 different ~~pBluescript~~ pBLUESCRIPT™ clones from each of the source library plates. The Condensed Plate was grown for 16 h at 37° C. and then used to inoculate two white 96-well Polyfiltronics microtiter daughter plates containing in each well 250 µL of LB Amp/Meth (without glycerol). The original condensed plate was put in storage -80° C. The two condensed daughter plates were incubated at 37° C. for 18 h.

Please replace paragraph [0261] on page 85 with the following amended paragraph:

[0259] Fifty µL of the '600 µM stock solution' was added to each of the wells of a white condensed plate using the BIOMEK™ ~~Biomek~~ to yield a final concentration of substrate of ~100 µM. The fluorescence values were recorded (excitation=400 nm, emission=505 nm) on a plate reading fluorometer immediately after addition of the substrate. The plate was incubated at 70° C. for 60 min. and the fluorescence values were recorded again. The initial and final fluorescence values were subtracted to determine if an active clone was present by an increase in fluorescence over the majority of the other wells.